

This listing of claims will replace all prior versions, and listings of claims in the application.

In the Claims:

1. (original) A method for detecting an isolate of a *B. cereus* group, in a sample, the method comprising:

- (a) placing on a microchip oligonucleotide probes targeted to rRNA sequences wherein at least one mismatch is sufficient to discriminate among the *B. cereus* subgroups;
- (b) providing conditions for hybridization of the probes with rRNA from the sample; and
- (c) analyzing hybridization signals in the microchip from which the particular isolate is detected.

2. (original) The method of claim 1, wherein the oligonucleotide probes are directed to 16S rRNA and 23S rRNA and the corresponding target sequences are shown in FIG. 1 and FIG. 2.

3. (original) The method of claim 1, wherein the probes are labeled.

4. (original) The method of claim 3, wherein the labels are selected from the group consisting of fluorescent dyes, radio isotopes, immunological labels, immuno-chemical labels and gold particles.

5. (original) The method of claim 1, wherein the oligonucleotide probes selected from the group consisting of sequences listed in Table 5 discriminate subgroups Anthracis, Cereus A, Cereus B, Thuringiensis A, Thuringiensis B, Mycoides A and Mycoides B.

6. (original) The method of claim 1, wherein pairs of oligonucleotide probes that discriminate subgroups *Anthracis* from *Cereus A* are ps21/ps22, ps23/ps24, 23F13/23F14, 23F15/23F16, and C9/C10.

7. (original) The method of claim 1, wherein a ratio of hybridization signals of oligonucleotide probes ps17 and ps18 discriminates between *B. anthracis* Ames and *B. cereus* 9620.

8. (original) The method of claim 1, wherein the oligonucleotide probes are ps21, ps22, ps23, and ps24 to discriminate *B. anthracis* Sterne from *B. cereus* HER 1414 and *B. thuringensis* B8.

9. (original) The method of claim 1, wherein the oligonucleotide probes are ps7,

ps8, and ps9 to discriminate *B. thuringensis* 4Q281 from other *B. cereus* subgroup isolates.

10. (currently amended) A microarray that comprises oligonucleotide probes selected from the group consisting of sequences designated: (SEQ ID NOS 70-95 respectively in order of appearance)

Oligonucleotide Name	5' to 3' Sequence
ps1	AGC TCT TAA TCC ATT CGC TC
ps2	AGC TCT cAA TCC ATT CGC TC
ps3	TAA CTT CAT AAG AGC AAG CT
ps4	TAA CTT CtT gAG AGC AAG CT
ps5	CCG CTA ACT TCA TAA GAG CA
ps6	CCG CTA ACT T Ct TgA GAG CA
ps7	GAA CCA TGC GGT TCA AAA TG
ps8	GAA CCA TGC aGT TCA AAA TG
ps9	GAA CCA TGC GGT TCA AAA TG
ps10	GcA CCA TGC GGT gCA AAA TG
ps11	CAA TTT CGA ACC ATG CGG TT
ps12	gAA TTT CG c ACC ATG CGG Tg
ps13	GCC TTT CAA TTT CGA ACC AT
ps14	GCC TTT gAA TTT CG c ACC AT
ps15	CGA AGC CGC CTT TCA ATT TC
ps16	CGA AGC CGC CTT TgA ATT TC
ps17	TCT AGG GTT GTC AGA GGA TG
ps18	TCT AGG GTT tTC AGA GGA TG
ps19	TCT GCT CCC GAA GGA GAA GC
ps20	TCT GC c CCC GAA GG g GAA GC
ps21	CAG CTC AGC CTT CAC GAT AA
ps22	CAG CTC AGC CTT tAC GAT AA
ps23	CAC TGA TAC CAT TG GTA TCA
ps24	CAC TGA TAC CAT TcG GTA TCA
ps25	CGGTCTTGCAGCTTTGTA
ps26	ATTCCAGCTTCACGCAGTC

11. (original) The microarray of claim 10, wherein the oligonucleotides are arranged in a specific pattern wherein I, II, III and IV are columns and A, B, C, D, E, and F

are rows in the microchip:

	<i>I</i>	<i>II</i>	<i>III</i>	<i>IV</i>
A	ps19	ps20	ps7	ps8
B	ps15	ps16	ps3	ps4
C	ps9	ps10	ps5	ps6
D	ps13	ps14	ps1	ps2
E	ps11	ps12	-	-
F	-	-	ps17	ps18

12. (original) A microarray as in claim 10, wherein the oligonucleotides are arranged in pairs: ps19 and ps20; ps15 and ps16; ps9 and ps10; ps13 and ps14; ps11 and ps12; ps7 and ps8; ps3 and ps4; ps5 and ps6; ps1 and ps2; ps17 and ps18.

13. (original) A microarray represented in FIG. 8.

14. (original) The microarray of claim 13, wherein the oligonucleotides are arranged in pairs: 23F1 and 23F2; 23F5 and 23F6; 23F7 and 23F8; 16A1 and 16A2; 16A3 and 16A4; 16A5 and 16A6; 16A7 and 16A8; 16A9 and 16A10; #54 and SB25; SB10 and SB11; A7 and A8; 23F3 and 23F4; SB23 and SB22; D1 and D2A; B1 and B2; B7 and B8; C5 and C6; C7 and C8; A3 and A4; 23F13 and 23F14; 23F15 and 23F16; SB22 and SB23; B11 and B12; C9 and C10; A1 and A2; A5 and A6; A9 and A10; A11 and A12.

15. (original) A microarray comprising oligonucleotide probes selected from the group consisting of sequences listed in Table 5.

16. (currently amended) A probe selected from the group consisting of sequences designated: (SEQ ID NOS 70-95 respectively in order of appearance)

Oligonucleotide Name	5' to 3' Sequence
ps1	AGC TCT TAA TCC ATT CGC TC
ps2	AGC TCT cAA TCC ATT CGC TC
ps3	TAA CTT CAT AAG AGC AAG CT
ps4	TAA CTT CtT gAG AGC AAG CT
ps5	CCG CTA ACT TCA TAA GAG CA
ps6	CCG CTA ACT TC t TgA GAG CA
ps7	GAA CCA TGC GGT TCA AAA TG
ps8	GAA CCA TGC aGT TCA AAA TG
ps9	GAA CCA TGC GGT TCA AAA TG

ps10	GeA CCA TGC GGT gCA AAA TG
ps11	CAA TTT CGA ACC ATG CGG TT
ps12	gAA TTT CGe ACC ATG CGG Tg
ps13	GCC TTT CAA TTT CGA ACC AT
ps14	GCC TTT gAA TTT CGe ACC AT
ps15	CGA AGC CGC CTT TCA ATT TC
ps16	CGA AGC CGC CTT TgA ATT TC
ps17	TCT AGG GTT GTC AGA GGA TG
ps18	TCT AGG GTT tTC AGA GGA TG
ps19	TCT GCT CCC GAA GGA GAA GC
ps20	TCT GCe CCC GAA GGg GAA GC
ps21	CAG CTC AGC CTT CAC GAT AA
ps22	CAG CTC AGC CTT tAC GAT AA
ps23	CAC TGA TAC CAT TG GTA TCA
ps24	CAC TGA TAC CAT TcG GTA TCA
ps25	CGGTCTTGCAGCTTTGTA
ps26	ATTCCAGCTTCACGCAGTC

17. (original) The probe of claim 16, wherein the sequence of the oligonucleotide probe is reversed.

18. (original) An oligonucleotide probe selected from the group consisting of sequences listed in Table 5.

19. (original) The probe of claim 18, wherein the sequence of the oligonucleotide probe is reversed.

20. (original) A diagnostic kit to detect *B. anthracis* target rRNA in a sample, the diagnostic kit comprising:

- (a) a microchip that comprises at least one oligonucleotide probe that distinguishes *B. anthracis I* from other closely related microorganisms; and
- (b) a method for detecting hybridization between the at least one probe and the target rRNA by which hybridization, *B. anthracis* is detected.

21. (original) A method for taxonomically classifying *B. cereus* groups, said method comprising:

- (a) developing strain- and subgroup-specific signature profiles of 16S and

23S rRNA sequences for *B. cereus* group isolates; and

- (b) using the signature profiles to construct phylogenetic trees in order to classify the various *B. cereus* group isolates.

22. (original) A 23S rRNA molecule selected from the group consisting of GenBank accession numbers AF267734, AF267876, AF267877, AF267880, AF267878, AF267879, AF267881, AF267885, AF267884, and AF267883.